

GP/1643

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/580,523

DATE: 08/30/2000

TIME: 13:47:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\08302000\I580523.raw

3 <110> APPLICANT: Zhou, Xiao-Mai
5 <120> TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
6 AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
7 THAT REGULATE APOPTOSIS
9 <130> FILE REFERENCE: A7483
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/580,523
C--> 12 <141> CURRENT FILING DATE: 2000-05-30
14 <160> NUMBER OF SEQ ID NOS: 20
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 168
20 <212> TYPE: PRT
21 <213> ORGANISM: Homo sapiens
23 <400> SEQUENCE: 1
24 Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
25 1 5 10 15
27 Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
28 20 25 30
30 Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
31 35 40 45
33 Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
34 50 55 60
36 Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
37 65 70 75 80
39 Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
40 85 90 95
42 Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
43 100 105 110
45 Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
46 115 120 125
48 Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
49 130 135 140
51 Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
52 145 150 155 160
54 Arg Gly Ser Ser Ala Pro Ser Gln
55 165
58 <210> SEQ ID NO: 2
59 <211> LENGTH: 204
60 <212> TYPE: PRT
61 <213> ORGANISM: Mus musculus
63 <400> SEQUENCE: 2
64 Met Gly Thr Pro Lys Gln Pro Ser Leu Ala Pro Ala His Ala Leu Gly
65 1 5 10 15
67 Leu Arg Lys Ser Asp Pro Gly Ile Arg Ser Leu Gly Ser Asp Ala Gly
68 20 25 30
70 Gly Arg Arg Trp Arg Pro Ala Ala Gln Ser Met Phe Gln Ile Pro Glu
71 35 40 45

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73 Phe Glu Pro Ser Glu Gln Glu Asp Ala Ser Ala Thr Asp Arg Gly Leu
74      50                      55                      60
76 Gly Pro Ser Leu Thr Glu Asp Gln Pro Gly Pro Tyr Leu Ala Pro Gly
77 65      70                      75                      80
79 Leu Leu Gly Ser Asn Ile His Gln Gln Gly Arg Ala Ala Thr Asn Ser
80      85                      90                      95
82 His His Gly Gly Ala Gly Ala Met Glu Thr Arg Ser Arg His Ser Ser
83      100                     105                     110
85 Tyr Pro Ala Gly Thr Glu Glu Asp Glu Gly Met Glu Glu Glu Leu Ser
86      115                     120                     125
88 Pro Phe Arg Gly Arg Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala
89      130                     135                     140
91 Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser Asp Glu Phe Glu Gly
92 145      150                     155                     160
94 Ser Phe Lys Gly Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln
95      165                     170                     175
97 Met Arg Gln Ser Ala Gly Trp Thr Arg Ile Ile Gln Ser Trp Trp Asp
98      180                     185                     190
100 Arg Asn Leu Gly Lys Gly Gly Ser Thr Pro Ser Gln
101      195                     200
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 162
106 <212> TYPE: PRT
107 <213> ORGANISM: Mus musculus
109 <400> SEQUENCE: 3
110 Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ala Ser
111 1      5                      10                      15
113 Ala Thr Asp Arg Gly Leu Gly Pro Ser Leu Thr Glu Asp Gln Pro Gly
114      20                      25                      30
116 Pro Tyr Leu Ala Pro Gly Leu Leu Gly Ser Asn Ile His Gln Gln Gly
117      35                      40                      45
119 Arg Ala Ala Thr Asn Ser His His Gly Gly Ala Gly Ala Met Glu Thr
120      50                      55                      60
122 Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr Glu Glu Asp Glu Gly
123 65      70                      75                      80
125 Met Glu Glu Glu Leu Ser Pro Phe Arg Gly Arg Ser Arg Ser Ala Pro
126      85                      90                      95
128 Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met
129      100                     105                     110
131 Ser Asp Glu Phe Glu Gly Ser Phe Lys Gly Leu Pro Arg Pro Lys Ser
132      115                     120                     125
134 Ala Gly Thr Ala Thr Gln Met Arg Gln Ser Ala Gly Trp Thr Arg Ile
135      130                     135                     140
137 Ile Gln Ser Trp Trp Asp Arg Asn Leu Gly Lys Gly Gly Ser Thr Pro
138 145      150                     155                     160
140 Ser Gln
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 26
145 <212> TYPE: PRT

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146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: BAD BH3
150 consensus sequence
152 <400> SEQUENCE: 4
153 Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser Asp Glu Phe
154 1 5 10 15
156 Val Asp Ser Phe Lys Lys Gly Leu Pro Arg
157 20 25
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 26
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Description of Artificial Sequence: BAK BH3
167 consensus sequence
169 <400> SEQUENCE: 5
170 Thr Met Gly Gln Val Gly Arg Gln Leu Ala Ile Ile Gly Asp Asp Ile
171 1 5 10 15
173 Asn Arg Arg Tyr Asp Ser Glu Phe Gln Thr
174 20 25
177 <210> SEQ ID NO: 6
178 <211> LENGTH: 26
179 <212> TYPE: PRT
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: BAX BH3
184 consensus sequence
186 <400> SEQUENCE: 6
187 Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys Arg Ile Gly Asp Glu Leu
188 1 5 10 15
190 Asp Ser Asn Met Glu Leu Gln Arg Met Ile
191 20 25
194 <210> SEQ ID NO: 7
195 <211> LENGTH: 26
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: BIK BH3
201 consensus sequence
203 <400> SEQUENCE: 7
204 Gly Ser Asp Ala Leu Ala Leu Arg Leu Ala Cys Ile Gly Asp Glu Met
205 1 5 10 15
207 Asp Val Ser Leu Arg Ala Pro Arg Leu Ala
208 20 25
211 <210> SEQ ID NO: 8
212 <211> LENGTH: 26
213 <212> TYPE: PRT
214 <213> ORGANISM: Artificial Sequence

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216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Artificial Sequence: BID BH3
218     consensus sequence
220 <400> SEQUENCE: 8
221 Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met
222   1           5           10           15
224 Asp Arg Ser Ile Pro Pro Gly Leu Val Asn
225           20           25
228 <210> SEQ ID NO: 9
229 <211> LENGTH: 26
230 <212> TYPE: PRT
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: HRK BH3
235     consensus sequence
237 <400> SEQUENCE: 9
238 Ala Ala Gln Leu Thr Ala Ala Arg Leu Lys Ala Leu Gly Asp Glu Leu
239   1           5           10           15
241 His Gln Arg Thr Met Trp Arg Arg Arg Ala
242           20           25
245 <210> SEQ ID NO: 10
246 <211> LENGTH: 26
247 <212> TYPE: PRT
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Description of Artificial Sequence: BOK BH3
252     consensus sequence
254 <400> SEQUENCE: 10
255 Arg Leu Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Asp Glu Leu
256   1           5           10           15
258 Glu Gln Ile Arg Pro Ser Val Tyr Arg Asn
259           20           25
262 <210> SEQ ID NO: 11
263 <211> LENGTH: 26
264 <212> TYPE: PRT
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Description of Artificial Sequence: BIM BH3
269     consensus sequence
271 <400> SEQUENCE: 11
272 Pro Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe
273   1           5           10           15
275 Asn Ala Tyr Tyr Ala Arg Arg Val Phe Leu
276           20           25
279 <210> SEQ ID NO: 12
280 <211> LENGTH: 25
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:

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285 <223> OTHER INFORMATION: Description of Artificial Sequence: BAD primer
286      (murine)
288 <400> SEQUENCE: 12
289 gcctccagga tccaagatgg gaacc                25
291 <210> SEQ ID NO: 13
292 <211> LENGTH: 23
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Artificial Sequence: BAD primer
298      (murine)
300 <400> SEQUENCE: 13
301 ggagcgggta gaattccggg atg                23
303 <210> SEQ ID NO: 14
304 <211> LENGTH: 25
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: BAD primer
310      (murine short)
312 <400> SEQUENCE: 14
313 tggagaccag gatcccagag tagct                25
315 <210> SEQ ID NO: 15
316 <211> LENGTH: 24
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Description of Artificial Sequence: Human PKI
322      primer
324 <400> SEQUENCE: 15
325 ctatgtggat ccttggtagc aatg                24
327 <210> SEQ ID NO: 16
328 <211> LENGTH: 24
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Description of Artificial Sequence: Human PKI
334      primer
336 <400> SEQUENCE: 16
337 cctcatagac cttaagtaaa caaa                24
339 <210> SEQ ID NO: 17
340 <211> LENGTH: 18
341 <212> TYPE: PRT
342 <213> ORGANISM: Homo sapiens
344 <400> SEQUENCE: 17
345 Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser Asp Glu Ser Val Asp
346   1             5             10             15
348 Ser Phe
351 <210> SEQ ID NO: 18

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VERIFICATION SUMMARY DATE: 08/30/2000
PATENT APPLICATION: US/09/580,523 TIME: 13:47:26

Input Set : A:\ES.txt
Output Set: N:\CRF3\08302000\I580523.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date